

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2000, 22:47:08 ; Search time 3292.45 Seconds
(without alignments)
3979.632 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000
Sequence: 1 cgcctcctacctaagtagagtc.....tgattgtcctaaacatttc 3000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

GenEmbl: *
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94: gb_vl2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	2775.8	92.5	2787	5 AB1835	AB1835 Sequence 9
6	2239.4	74.6	2241	1 AB033795	AB033795 Chlamydia
7	546.6	18.2	4926	2 CP072499	U72499 Chlamydia
8	531.8	17.7	12676	1 AE002192	AE002192 Chlamydia
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us-09-428-122-1.rge

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2999; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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1 (sites)
AUTHORS
Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K., Shirai,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T.
TITLE
Comparison of whole genome sequences of chlamydia pneumoniae J138 from japan and CWL029 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
JOURNAL
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MEDLINE
2 (bases 1 to 300050)
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Shirai,M.
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Direct Submission
TITLE
Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi 755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp, Tel.:81-836-22-2227, Fax:81-836-22-2415)
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AB033780-AB033781, AB033792-AB033799: Submitted (25-Oct-1999)
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 ORGANISM Chlamydomophila pneumoniae (strain:J138) DNA.
 Bacteria: Chlamydiales; Chlamydiaceae; Chlamydomophila.
 REFERENCE 1 (sites)
 AUTHORS Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M.,
 Takeuchi,A., Nishida,J., Shibata,K., Fujinaga,R., Yoneda,H.,
 Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A.,
 Ishii,K., Shiba,T., Hattori,M. and Kihara,S.
 TITLE Comparison of outer membrane protein genes omp and pmp in the whole
 genome sequences of Chlamydia pneumoniae isolates from Japan and US
 JOURNAL Unpublished (1999)
 REFERENCE 2 (bases 1 to 2241)
 AUTHORS Hirakawa,H. and Shirai,M.
 TITLE Direct Submission

JOURNAL

Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases. Hideki Hirakawa, Kyushu University, Graduate School of Genetic Resources Technology; 6-10-1 Hakozaki, Higashi-ku, Fukuoka, Fukuoka 812-8581, Japan (E-mail: hirakawa@grt.kyushu-u.ac.jp, URL: http://www.grt.kyushu-u.ac.jp, Tel: 81-92-642-3043, Fax: 81-92-642-3043)

FEATURES

SOURCE

Location/Qualifiers

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GAIKDF

BASE COUNT 660 a 474 c 478 g 629 t

ORIGIN

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Chlamydomophila pneumoniae (strain:J138) DNA.
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Chlamydomophila pneumoniae
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydomophila.
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1 (sites) Shiral,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K.,
Shiba,T., Ishii,K., Hattori,M., Kuzhar,S. and Nakazawa,T.
Comparison of whole genome sequences of chlamydia pneumoniae J138
from Japan and CMV029 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
2 (bases 1 to 300600)
Shiral,M.
REFERENCE
Direct Submission
Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Mitsunori Shiral, Yamaguchi University School of Medicine,
Department of Microbiology, 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8505, Japan (E-mail:mshiral@po.cc.yamaguchi-u.ac.jp,
Tel:81-836-22-2227, Fax:81-836-22-2415)
AB033782-AB033785, AB033800-AB033815: Submitted (25-Oct-1999)
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AB036079-AB036082: Submitted (18-Dec-2000).
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ACCESSION AE001628 AE001363
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  Grimwood, J., Davis, R.W. and Stephens, R.S.
  Comparative Genomes of Chlamydia pneumoniae and C. trachomatis
  Unpublished
  2 (bases 1 to 10757)
  Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
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  Direct Submission
  Submitted (01-DEC-1998) Program in Infectious Diseases, University
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SOURCE	unclassified.													
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AUTHORS	Madsen, A. and Birkelund, S.													
TITLE	NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE													
JOURNAL	Patient: WO 9858953-A 30-DEC-1998.													
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 ORGANISM Chlamydia pneumoniae.
 REFERENCE 1 (bases 1 to 17280)
 AUTHORS Boesen, T.
 JOURNAL Direct Submission
 TITLE Submitted (21-Jan-1999) Boesen T., Department of Medical Microbiology and Immunology, University of Aarhus, The Bartholin Building, DK-8000 Aarhus, DENMARK
 REFERENCE 2 (bases 1 to 17280)
 AUTHORS Hierno, K., Boesen, T., Daugaard, L., Knudsen, K., Madsen, A., Christiansen, G., and Birkelund, S.
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 Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
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 Direct Submission
 Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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6	522.2	17.4	2757	20	Chlamydia pneumoni
7	515	17.2	2787	20	Chlamydia pneumoni
8	514	17.1	2793	20	Chlamydia pneumoni
9	506	16.9	3000	20	Chlamydia pneumoni
10	465.8	15.5	3200	20	Chlamydia pneumoni
11	389	13.0	3050	21	DNA encoding the C
12	378.4	12.6	2838	20	Chlamydia pneumoni

13	340.2	11.3	2526	20	X06819	Chlamydia pneumoni
14	273.2	9.1	3052	20	X06818	Chlamydia pneumoni
15	243.4	8.1	3150	21	A27342	Chlamydia POMp1B
16	209.2	7.0	1830	20	X06830	Chlamydia pneumoni
17	197.6	6.6	840	20	X06824	Chlamydia pneumoni
18	140.6	4.7	3354	20	X60556	Seq ID No: 23 of W
19	133.8	4.5	3324	20	X60557	Seq ID No: 24 of W
20	132.2	4.4	4435	20	X60539	C. trachomatis LGV
21	130.6	4.4	1444	20	X60547	C. trachomatis HMW
22	104	3.5	1200	20	X06829	Chlamydia pneumoni
23	80.8	2.7	1545	20	X06825	Chlamydia pneumoni
24	50.4	1.7	1511	20	X60546	C. trachomatis HMW
25	50.4	1.7	1515	20	X60555	Seq ID No: 22 of W
26	46	1.5	787	20	X06826	Chlamydia pneumoni
27	43.4	1.4	1038602	20	201425	Complete genome se
28	42.4	1.4	3975	9	N81157	Malaria-specific 9
29	42.4	1.4	3975	13	Q2299	SERP gene. Plasm
30	42.4	1.4	6124	11	Q03568	Sequence encoding
31	41	1.4	1497	21	256377	Escherichia coli f
32	41	1.4	1689	8	N70495	Sequence of Escher
33	41	1.4	2108	10	N91116	Flagellin gene of
34	41	1.4	2109	8	N70985	E. coli flagellin 9
35	39.6	1.3	580073	18	T58840	Mycoplasma genital
36	37.6	1.3	2963	18	T93775	PSD-93 coding sequ
37	36.8	1.2	1269	19	V12774	Metal-regulated tr
38	36.4	1.2	1598	20	X85043	Human secreted pro
39	36.2	1.2	1300	21	261504	DNA encoding the C
40	36.2	1.2	3050	21	261586	Nucleotide sequenc
41	36	1.2	2610	13	Q32556	LEMM1 8 CDNA. Lyc
42	35.8	1.2	1951	16	Q94449	Bacterial transfer
43	35.8	1.2	1951	18	T49507	Transferin recept
44	35.8	1.2	1951	19	V21443	H. influenzae stra
45	35.8	1.2	1951	21	289171	H. influenzae non-

ALIGNMENTS

RESULT 1	
ID A27021	standard; DNA: 3000 BP.
AC A27021:	
DT 11-AUG-2000	(first entry)
XX	Chlamydia pneumoniae 98kD putative outer membrane protein gene.
DE	Chlamydia pneumoniae 98kD putative outer membrane protein; ds.
XX	Chlamydia; antigen; vaccine; infection; outer membrane protein; ds.
KM	Chlamydia; antigen; vaccine; infection; outer membrane protein; ds.
XX	Chlamydia pneumoniae.
OS	Chlamydia pneumoniae.
XX	
FH Key	Location/Qualifiers
FT CDS	101..2887
FT	/*tag= a
FT	/product= "98kDa putative outer membrane protein"
XX	
PN W0200026237-A2.	
XX	
PD 11-MAY-2000.	
XX	
PF 29-OCT-1999;	99WO-GB03579.
XX	
PR 29-OCT-1998;	98US-0106070.
PR 01-MAR-1999;	99US-0122066.
PR 27-OCT-1999;	99US-0428122.
XX	
PA (CONN-) CONNAUGHT LAB LTD.	
XX	
PI Murdin AD, Oomen RP, Dunn PL;	
XX	
DR WPI: 2000-365569/31.	
DR P-PSDB: Y94327.	

XX Novel Chlamydia 98 kDa putative outer membrane protein antigen, used
PT for vaccination and protection against Chlamydia infection
PS Claim 1; Fig 1; 93pp; English.
XX The present sequence is the 98kDa putative outer membrane protein gene
CC from Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
CC contains the sequence encoding the C-terminal sequence of the putative
CC outer membrane protein and a BstXI restriction site. The stop codon was
CC excluded and an additional nucleotide was inserted to obtain an in-frame
CC C-terminal fusion with the Histidine tag. The PCR product was cloned
CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
CC the vector and the PCR product with NotI and BamHI and performing a
CC ligation reaction. This expression vector was injected intramuscularly
CC and intranasally into mice, which were subsequently inoculated with
CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
CC were lower than those of the controls. Thus the 98kDa putative outer
CC membrane protein can be used as a vaccine to provide protection against
CC Chlamydia infections, especially Chlamydia pneumoniae infections.
CC The polypeptide may also be administered orally to treat Chlamydia
CC infection. The present sequence may also be used in the
CC construction of attenuated Chlamydia strains that can over-express the
CC gene or express it in a non-toxic form.
XX
XX Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;
SQ

Query Match 100.0%; Score 3000; DB 21; Length 3000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 cgcctctactagtagaggttgaggaattcttgactgtttccctatgtgtatct 60
QY 61 cttaaatatataatcaaaaagtagatataatttacaataagaagctctctcccaa 120
Db 61 cttaaatatataatcaaaaagtagatataatttacaataagaagctctctcccaa 120
QY 121 gtttgatatttctacattgtctatcttcccttgctcatattgctacagagcaagtttt 180
Db 121 gtttgatatttctacattgtctatcttcccttgctcatattgctacagagcaagtttt 180
QY 181 ggtttcaagtcgaggttcgattgggaataaaatgtgaattttcagttcgtgagatca 240
Db 181 ggtttcaagtcgaggttcgattgggaataaaatgtgaattttcagttcgtgagatca 240
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QY 361 aggttaacgggaactctctattgttccaacagtcgattgcaaggactgtgacagggctgc 420
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QY 481 tattgcgtctcctggaagttcgataactacggcgaaggagccgttagtctgctacaggg 540
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QY 541 tagcttgagttgacaaaaaatgtcagttgtctctcagcaaaaactttcaacgagataa 600
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Db 541 tagcttgagttgacaaaaaatgtcagttgtctctcagcaaaaactttcaacgagataa 600
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Db 601 tggggggtgcataccgcgcaaaaactcttcatataacaggagataaatgtcagctcgtt 660
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RESULT 2
X91990
ID X91990 standard; DNA; 1230025 BP.
XX
AC X91990;
XX
DT 13-SEP-1999 (first entry)
XX
DE Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; ss.
XX
OS Chlamydia pneumoniae.
XX
PN MO9927105-A2.
XX
PD 03-JUN-1999.
XX
PE 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST ) GENSET.
XX
PI Griffiths R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Claim 1: Page 291-611; 1912pp; English.
XX
CC The present sequence represents the complete genome of Chlamydia
CC pneumoniae, and encodes proteins Y34584-Y35879. C. pneumoniae causes
CC respiratory disease such as pneumonia and bronchitis and is thought
CC to be a contributing factor in heart disease, sarcoidosis, sinusitis,
CC purulent otitis media, erythema nodosum or pharyngitis. The polypeptides
CC encoded by the open reading frames of the C. pneumoniae genome (see
CC Y34584-Y35879) can be used in immunogenic compositions as vaccines.
CC Vectors containing C. pneumoniae nucleotide sequences can also be
CC used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;

Query Match 99.28; Score 2975.4; DB 20; Length 1230025;
Best Local Similarity 99.98; Pred. No. 0;
Matches 2998; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 cgccttaccatgagaggtgagtgatattcttgcattgttctcctattgtgtatct 60
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Db 31658 cgccttaccatgagaggtgagtgatattcttgcattgttctcctattgtgtatct 31717

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QY 61 ctttaataatcattcaataaatacgaatataatttcaatgaaagctctcttcccaa 120
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QY 301 aacagggcaacgaatcacaataaagctgttttaacaacactaagggggaattgactttcac 360
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Db 31958 aacagggcaacgaatcacaataaagctgttttaacaacactaagggggaattgactttcac 32017
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Db 32078 tgttaacagcgagctgtggttagaataatcacaacgtttataggggttctctcgctactctt 32137
QY 481 tattgcgtctctcggaagcttcgaataacacggcaaaagagcggttagcgtctactacgg 540
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Db 32198 taagcttaagcttgcaaaaatgtaattgtcttcttcaagcaaaaacttttcaacgggataa 32256
QY 601 tggcggtgctatcaacggcaaaaactcttcatcaacaggggactacaatgtgcagctcgtt 660
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QY 721 tactggaaaacaaagggaagctctcttcttctgacaatactctctggaattctggaactgc 780
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Db 32557 ttataaaactagtaacgaatacgaatgccaacactgtaaaatcagaatttctctctcag 32616
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QY 1141 ctttttagggaatacagctcaccttctactactctgtggaacgaatagaatgactt 1200
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Oy 3000 c 3000
Db 34657 c 34657

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RESULT 3
X06820
ID X06820 standard: DNA: 2787 BP.

XX X06820;
XX 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp8 DNA.
XX
KW Omp8; Outer membrane protein 8; surface exposed protein; antigen;
XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
OS Chlamydia pneumoniae.
XX
XX W09858953-A2.
XX

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PD 30-DEC-1998.
XX
XX '19-JUN-1998; 98NO-DK00266.
XX
XX 23-JUN-1997; 97DK-0000744.
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XX (BIRK/) BIRKELUND S.
XX (CHR1/) CHRISTIANSEN G.
XX
XX Birkelund S, Christiansen G, Knudsen K, Madsen A;
XX Mygind P;
XX WPI: 1999-105610/09.
XX DR P-PSDB; W88421.
XX
XX Species-specific test for identifying mammals infected with
XX Chlamydia pneumoniae - comprises detecting antibodies specific for
XX outer membrane proteins of C. pneumoniae or nucleic acids encoding
XX these proteins
XX
XX Claim 6; Page 52-53; 115pp; English.
XX
XX This DNA sequence codes for the novel 90.0 kDa surface exposed
XX protein Omp8 (see W88421) of the human respiratory pathogen
XX Chlamydia pneumoniae. By generating antibodies against C.
XX pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
XX was obtained which reacted with outer membrane proteins. The
XX antibody was used to identify the genes (see X06816-27) encoding
XX Omp4-Omp5 proteins (see W88417-28) in an expression library of
XX C. pneumoniae DNA. The genes are situated in 2 gene clusters:
XX Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
XX the other, and encode polypeptides of about 89.6-100.3 kDa and
XX about 56.1 kDa. The invention provides a new species specific test
XX for identifying mammals (including humans) infected with Chlamydia
XX pneumoniae. The test comprises detecting antibodies specific for
XX Omp4-Omp5 or detecting nucleic acid fragments encoding these outer
XX membrane proteins, especially by PCR. The proteins are also used
XX in the diagnosis of C. pneumoniae infection in mammals. The
XX nucleic acids and proteins can also be used in the immunization of
XX mammals, the nucleic acids being particularly useful as DNA
XX vaccines for effecting in vivo expression of antigens. The
XX vaccines may also prevent atherosclerosis and bronchial asthma,
XX which are possibly associated with C. pneumoniae.
XX
XX Sequence 2787 BP; 811 A; 583 C; 598 G; 795 T; 0 other;
XX
XX Query Match 92.5%; Score 2775.8; DB 20; Length 2787;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 2780; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Oy 101 atgaagctctctccccaagttgtattcttctacattgtctattcccttgcctatg 160
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Oy 161 atgctacacgagacagtttggattcaagtgcgagtttcgattggaaataaagtgtat 220
Db 61 atgctacacgagacagtttggattcaagtgcgagtttcgattggaaataaagtgtat 120
Oy 221 ttctcaattgctgagatcaggaagatcgtgcgaactcctcattttaaggaaatgctc 280
Db 121 ttctcaattgctgagatcaggaagatcgtgcgaactcctcattttaaggaaatgctc 180
Oy 281 actctagaaataatctctgcgaacagcgacagcaatcacaagaagcttttaacaacact 340
Db 181 actctagaaataatctctgcgaacagcgacagcaatcacaagaagcttttaacaacact 240
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Db 241 aagggcatttgacttccacaggaacggaactctctattgtccaaagctgtgatgca 300
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QY	2614	ggaaatcagactgcagaaagatgcacagctacaactaaactctgtgttaactgtgatatctgtgt	2673b
Db	2514	gtctctgattgttaigtactcttctcttaigtatcgtacgtactatccatgtctcgtactat	2573b
QY	2674	tgtgtgttaacccgcgactgctgcgaacaactgcgaatttagcgttgattcttggaaacct	2733b
Db	2574	cgcgaatgatcccaaatgcatctacagactgttaacagcggagccgactcttggaaactta	2633b
QY	2734	cgttacgattctggcaagaagaagctttagtccctgtgcgtgagggaaacacttttgctttaa	2793b
Db	2634	tgcacataacttagcaagaagagccttgcaagtgcgtgcagacgaactcaacgctcttc	2693b
QY	2794	ctcaaatcttgaagccctttagcccaatttctttgaattgcgtgtgcatctgcgaatta	2853b
Db	2694	tactatgtttgaagtgtcgtcgccagatttctttagaagtcgtgatccctcagagattta	2753b
QY	2854	caatgtagacttagagacaaatacaaatctta	2886b
Db	2754	taatgtatgactctgggggtgaattccaattcta	2786b
RESULT	5		
XX	261509		
ID	261509	standard; DNA; 2957 BP.	
AC	261509;		
XX	19-JUN-2000	(first entry)	
DT			
XX			
DE		DNA encoding the CPN100395 polypeptide.	
XX			
KW	CPN100395; Chlamydia infection; immune response; vaccine; ss.		
XX			
OS	Chlamydia pneumoniae.		
XX			
Key		Location/Qualifiers	
FF	101..2857		
FT	/*tag= a		
XX			

[illegible]

QY	602	gggggtgctatcacacggcaaaaactctttctatcaacgggagctacaatgtcagctctgtt	661
DB	605	ggggggagccatcaactaactgaagagactctgtctcttgacctgggagtagcoggttttagtcgttc	664
QY	662	tcctgaataactctctcccaagaagaaggcgagacatccagacttcgacttgcctccatctt	721
DB	665	cttggcaatagctctgcgcacaagaaggggagagcatctatgcctctcgggagctctgtgatt	724
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DB	725	tcctgagaatctcaggaatctctgagctcttcgcgaacaacagacgagcaacaactgaagcgcg	784
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QY	1022	ggagagacttaaccattctcagtataaatagtgtcacaatagagaggtgaacgcctccataaggtga	1081
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QY	1496	actcaaacagagcagattctcgtctcgcgaatagggcgtatggagacacactctga---acctact	1552
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DB	1535	gaggggggtcactctcaatgtcgccatgacatataatagattcctcttagatgaggcaataataa	1594
QY	1613	gcaanaatagaaacccaagagtagtgcataaaaaactgcagctttctcggaaacataactta	1672
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Db 2714 ttgctagacaagctctcttctgtacgtcgtgaatcatcatgcttcttcaacttt 2773
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Db 2774 gaatttccactcaggttgaagtcagatgcagaggtctctctcgtatgcatgcat 2833
QY 2864 ttaagagcaaataccacttaatgc 2890
Db 2834 ctgagagaagattcggattttaatcc 2860

RESULT 6
X06821
ID X06821 standard; DNA; 2757 BP.
XX
AC X06821;
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp9 DNA.
XX
KW Omp9; outer membrane protein 9; surface exposed protein; antigen;
KM infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
PN W0858953-A2.
PD 30-DEC-1998.
PE 19-JUN-1998; 98WO-DK00266.
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHRT/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Myind P;
XX
DR WPI: 1999-105610/09.
DR P-PDB: W06822.
XX
PT Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX
PS Claim 6: Page 55-56; 115pp; English.
XX
CC This DNA sequence codes for the novel 96.7 kDa surface exposed
CC protein Omp9 (see W88422) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see X06816-27) encoding
CC Omp4-Omp15 proteins (see W88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
XX
XX Sequence 2757 BP; 770 A; 564 C; 642 G; 781 T; 0 other:

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Query Match 17.4% Score 522.2: DB 20: Length 2757:
Best Local Similarity 53.4%: Pred NO. 1.3e-134:
Matches 1424: Conservative 0: Mismatches 1153: Indels 90: Gaps 12:

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DB 217 aaacaaacagacttaaccacaagctgttttcttaacacacgcaggaatcttcctcta 276
QY 362 gtaacggaactctctatgtttccaaacgctgagtcgaggagctgaaggcgctgt 421
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RESULT	7
ID	X06822
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AC	X06822;
XX	
DT	26-APR-1999 (first entry)
XX	
DE	Chlamydia pneumoniae surface exposed protein Omp10 DNA.
XX	
KW	Omp10; outer membrane protein 10; surface exposed protein; antigen;
XX	
KW	infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX	
OS	Chlamydia pneumoniae.
XX	
PN	W09858953-A2.
XX	
PD	30-DEC-1998.
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PF	19-JUN-1998; 98WO-DK00266.
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PR	23-JUN-1997; 97DK-0000744.
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PA	(BIRK/) BIRKELUND S.
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PA	(CHRT/) CHRISTIANSEN G.
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PI	Birkelund S, Christiansen G, Knudsen K, Madsen A;
XX	
PI	Mygind P;
XX	
DR	WPI; 1999-105610/09.
XX	
DR	P-PDB; W88423.
XX	

PT Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of *C. pneumoniae* or nucleic acids encoding
PT these proteins
XX
ES Claim 6; Page 59; 115pp: English.

h.

CC This DNA sequence codes for the novel 98.4 kDa surface exposed
CC protein Omp10 (see W884423) of the human respiratory pathogen
CC *Chlamydia pneumoniae*. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see X06815-27) encoding
CC Omp4-Omp15 proteins (see W88417-28) in an expression library of
CC *C. pneumoniae* DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with *Chlamydia*
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of *C. pneumoniae* infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with *C. pneumoniae*.

Sequence 2787 BP; 815 A; 689 C; 535 G; 748 T; 0 other;

Query Match	17.28;	Score 515;	DB 20;	Length 2787;
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Best Local Similarity 53.3%; Pred. No. 1.3e-132;
Matches 1425; Conservative 0; Mismatches 1175; Indels 75; Gaps 13

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QY	783	ttttacagaagctcgtgtgactatttctataatgtaatgtaaatcttctattatgacata	842

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QY 2853 acatgttagacttaggaagcaaaatacaacttctaa 2887
DB 2753 acaatgagatcttgaaggttaagttccagttctaa 2787

RESULT 8
X06823

ID X06823 standard; DNA: 2793 BP.
XX
AC X06823:
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp1 DNA.
XX
KW Omp1: outer membrane protein 11; surface exposed protein; antigen;
infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
PN WO9858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PI (CHRI/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Myind P;
DR WPI: 1999-105610/09.
XX P-PSDB: W88424.
XX
PS Claim 6: Page 62-63; 115pp; English.
XX
CC This DNA sequence codes for the novel 97.6 kDa surface exposed
CC protein Omp11 (see W88424) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see X06816-27) encoding
CC Omp4-Omp13 proteins (see W88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other. and encode polypeptides of about 89,6-100,3 kDa and
CC about 56,1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp13 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
XX
XX Sequence 2793 BP; 803 A; 681 C; 567 G; 742 T; 0 other:
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Query Match 17.1%; Score 514; DB 20; Length 2793;
Best Local Similarity 52.7%; Pred. No. 2,4e-132;
Matches 1404; Conservative 0; Mismatches 1200; Indels 60; Gaps 11;
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OY 601 tggcgtgtctatcacgcgaacaaactcttcaatcaacaggaatacaatgctcgtgt 660
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Db 2172 --catgcccattttggaagratcacgcgacatgtgtaagatattcctcattttgaa 2228
QY 2236 aggaaccttagctacacccatacagatagatctgaaacaaagttatacaactatcc 2385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2229 tgcacagctaaagctacacatacaaaaatgatatgatactcgtctataactctatcc 2288
QY 2386 tactgttaaggaagctggggagaaatgatagtttcgcttaagaattcgttga---gagc 2442
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2289 tgaagctcaaggttcttggaacataatctcgtgggtctcagagcctgggggtctcctg 2348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2443 tccgatttgcttagtgaagagtgctctatttagcagatgacatgcccctcattgaattga 2502
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2349 tctatatctccctaaagagacgcgtctctccagagatattcctcattttaaaatcca 2408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2503 gttgtctatgcacatcaggaaggttttaagaacaggaacagagactcggtatttg 2562

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Db 2409 ggcagtlctacgcgcgcacaaactttaagaagagtggtcgtgagccgtgtcttga 2468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2563 aagtacgcgtctgttgaattctgtccttactcattacgtgagatccgatttgaagaatcaga 2622
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2469 tgatgagacactagtgaaactgtctatccctcgtcgcactcgtttagaanaaatctcga 2528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2623 ctgcgaagatgcaagtgacaatctactccttggtatctgttgaattctgttgaatga 2682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2529 agatgaaaaaaataattctcgagattcctctagccaacttggtatgtatcgtataaaa 2588
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2683 cccgcactgtacgacaacacgcggaattagcgttattcttggaaaacttcgtagca 2742
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Db 2589 tcccgttcgctactctcctaattgtcagtgagagcctctcgtgacttgcatagtaaaaa 2648
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QY 2743 ttggaagacacagctttagtctcctcgtgcagggagacattttgtcttaactcaatt 2802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2649 cctcgacagacagcctctcttagcagatgctggaagccatctgactctctccctcatgt 2708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2803 tgaagccttagcccaatttcttcttgaattcgttggtcgtcactgcgaattcaatgtaga 2862
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Db 2709 agaactctcgtgggaagcgtcttatgagctcgtggtccagacacacatacaatgtaga 2768
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2863 cttaggaacaaaataccaattcta 2886
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2769 ttgtggttaagatactactcta 2792
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
X06828
ID X06828 standard; DNA; 3000 BP.
XX
AC X06828;
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omps DNA.
XX
KW Omps; outer membrane protein 5; surface exposed protein; antigen;
infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
FT CDS
FT CDS 259..3000
FT CDS /*tag= a
XX
PN W09858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK0266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHR1/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mylnd P;
XX
DR WPI: 1999-105610/09.
DR P-PSDB: W88429.
XX
XX Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX
XX Disclosure: Page 73-77, 115pp; English.
XX
XX This DNA sequence encodes the novel surface exposed protein Omps
CC (see W88429) of Chlamydia pneumoniae, a human respiratory pathogen.

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CC It is described as a subsequence of a claimed nucleic acid fragment
CC (see X06817) encoding Omp5 (see W8418). The invention provides a
CC new species specific test for identifying mammals (including
CC humans) infected with *C. pneumoniae*. The test comprises detecting
CC antibodies specific for surface exposed proteins Omp4-Omp5 (see
CC W8417-28) or detecting for nucleic acid fragments encoding them (see
CC X06816-27), especially by PCR. The proteins are also used in the
CC diagnosis of *C. pneumoniae* infection in mammals. The nucleic acids
CC and proteins can also be used in the immunization of mammals, the
CC nucleic acids being particularly useful as DNA vaccines for
CC effecting in vivo expression of antigens. The vaccines may also
CC prevent atherosclerosis and bronchial asthma, which are possibly
CC associated with *C. pneumoniae*.

XX Sequence 3000 BP; 867 A; 597 C; 658 G; 878 T; 0 other;

Query Match 16.9%; Score 506; DB 20; Length 3000;
Best Local Samlarity 52.6%; Pred. No. 4,1e-130;

Matches 1383; Conservative 0; Mismatches 1170; Indels 75; Gaps 10;

OY 247 tgcgtgaactactcctcatttaagggaatgtcacctagaanaatatcctgacagc 306
DB 414 tactggaatgaactactactgacagagataataactctgcaaaccttgagctgg- 472
OY 307 cacagcaatcacaaaagctgttttaacacacgctagggcgatttgacttccaggtaa 366
DB 473 --cagcttaacgaagggtgtttctctgacactcgaactctttaagcttgcgcgtga 530
OY 367 cgggaactctctatgtgtccaaacggtgagtcaggaactgaagagggctgcgttaa 426
DB 531 ggggactcactcttcttttaaatattagctagctgtaaggcgagacttctcgt 590
OY 427 cagcagcgtgtgtagtaattacacagcttaataaggttcttcgtctattttatgac 486
DB 591 tacaactgataaaatcgtctgactaacaggaatttcgagttcttacttcttaagcgccc 650
OY 487 gtctcttgaaagctcgaataactacgcgcaagagcgctgacgctcctaaggttagctt 546
DB 651 atcatcggttaatcacaaacccctcgaagaaaggtgcagtttaagtggagggatc---t 707
OY 547 gagtttgcaaaaatgtcagttgtctcttcagcaaaaacttttcaacggtataatggcg 606
DB 708 tacatttgatacaatggaactatttatttaaacagattactgtaggaanaatggcg 767
OY 607 tgcataccccaanaactcttcataaacagggagactacaatgccaactcgttttctga 666
DB 768 agccatttctcacaagaactcttcttgaaaaaacagacagcggaactccttcttgaag 827
OY 667 aaata-----ctctcctcaagaagaagcggaacatcagaactcgcagtccttac 717
DB 828 gaataaactcgacgcaacaggaanaaagtggtgctattgtctacttgtagtactaga 887
OY 718 catcactggaacccaagggaggtctcttttctgacaataactctcggatctctgagc 777
DB 888 tattacaataatcgcgtcctcactcctctctcgaacaaatgtgtlaagctcaggtg 947
OY 778 tgcgaattttacaggaactcgtgtgactattcttaataatgcttaagttcccttattga 837
DB 948 agctataaatagcacaggaactgtataactacaggaataagctctctgtattcttga 1007
OY 838 caataaggtcacagggagcgtcctcctcaacaacggggatagttcagaggtgctatctg 897
DB 1008 aaatagtgtagc---agcgacgcgaggaatgtagagagctcttctcgagatgacg---- 1060
OY 898 tgcattaaactagtaacagatacagtaagtcacccactcgaactgaacatgttactctt 957
DB 1061 -----atgttaccatatctgggaacacagaagttaacttt 1094
OY 958 cagcaacaatatacgcacaacagcgaggagagctatcatgtgaaaaagctcgaaatggc 1017
DB 1095 ctcaaggaacacagcgtgtagctaatgtagcgagcatttatgtcagaagaacttaactggc 1154

OY 1018 ttccggagga-----cttaccattcagtagaataagtgtaabtgaggtacagctcc 1071
DB 1155 ttccgggggggggggggttactctcttcttcaaaaatagatccaaaggtaccctgaag 1214
OY 1072 taaagttgagccataagctacgcagaatagtggggaattgagttatccgcgagatgtg 1131
DB 1215 taatggtgagccattctctatcactgcgagctggaaggtgtagtcttcttcaagaagaag 1274
OY 1132 tgaactgtctttttaggaataacagctcacttactactc---tggaagataagag 1188
DB 1275 ggaacttacccttcaatggtgattccattgttgcaactacacccaactcaaaaagaa 1334
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DB 1455 tctcaataaagcctgatacgaggtatagtaacagatlaagtggtcgatgttttctg 1514
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DB 1515 tgaagaagctctcgaagatgtaagcaaaagttagagcaacccctcaactccacgtgaaga 1574
OY 1429 gctctgtaactcttccaggaagtactctatctttaaacaatgagtagtcttgcagctca 1488
DB 1575 gctctgtaactcttcaactgcaggaatattagttacttaaacgtgtgtcactctgatacga 1634
OY 1489 ggcattcaactcacaagcagagatctcgtctcgaatgagcgtgaggaactcactcgaac 1548
DB 1635 aggtcttactcagacccggcggtctctcctgtatttaaggatggcgacaaacgttlaaagc 1694
OY 1549 ---tgctgatactagacacataaacaatttggcttaacaacagattcttatagcgtgac 1605
DB 1695 aagtaagagggagtgacttaacttaacaggtcttccacttctcgttagctcttttagggag 1754
OY 1606 aagaagggcaaaaatagaaacaaagctcagtcacaaaactcgtacttaactcgtgaacat 1665
DB 1755 taagaaagctgtgaattgtcgtctctgcagcaagtaaaaatgagcccttaagtggtccgat 1814
OY 1666 caatttatggaccggacggcagcttttatagaataatcagtttaagaataatccctcagtc 1725
DB 1815 tctcttttggataaccaggggaatgcttatgaaataatcagacttaggaanaaacccaaga 1874
OY 1726 ctaagacatcttaggctcaaaagctcttggaaactgaaacgacacggcagtgactcaga 1785
DB 1875 ctttcaatttggcagctctcgtcctgtgactcgaacaactacagatgtgtccagcggt 1934
OY 1786 tccataatgggttgggaattcctacttaagcgtatcagaatgaaggaacttggggccaattgttg 1845
DB 1935 tccataagtagaactcctcagcactatggttatccaagaatgactcgtgggaatgagttggt 1994
OY 1846 gg-----ggacaaggggtcttcaacgactgcaaccttcaactgagactaaacgg 1893
DB 1995 tgatgataccgcaagcactccaagaactaagaactaagaacagcgacattagcttggacaataacag 2054
OY 1894 ctatatctcattcccgcggtatcgcgtctctttagtccctaataagcttatggaatgact 1953
DB 2055 ctactctcggatcctgagcgltcaagggcctttagtctcctaataagccttgggagatctt 2114
OY 1954 tataataatgctctcccatctatctatgaggaactgcaaacgaagaaggttgcagggaga 2013
DB 2115 ttcagacatccaagagatccaaggtgtcatatagaagaagtgcttgaactcttgttllaga 2174
OY 2014 ccgtgcttttggtgtgctgtagtatcctaactcttccataaagatagtaacaacaacg 2073
DB 2175 tctgaagcttctgggctggtgagtgctgcgaattctttagataaagataagaaggggagaa 2234
OY 2074 aagcggttgcacatttgagtggtgttatgtcatagaggaacactacatacttcttgc 2133

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Db 2235 acgcaaatccgcatacaaaatctggtgatatctatccgaggtgcgcgcaactgttc 2294
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Db 2295 tgaataacttaattagcttggccttttgcgaactcttctgttgcgaataattccttagt 2354
Oy 2194 agcttaagaaatgacagctctacgaggaactctctatccagcaagaagaaacct 2253
Db 2355 cgttaaaaatactacgatacctatgcagagcctctctatcccaagacattacagaatg 2414
Oy 2254 tatctctctctcctgcaactacgagcctgtctgtcttcttctgttcccaagagattcc 2313
Db 2415 tagtggttcataagttgtctc--cttagataaactctcgtccttggagtcataaacc 2471
Oy 2314 tgtctctcttcaggaagaacttagtaccaccaatacgaataacgactctaaaccagta 2373
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Oy 2374 tacaacatacctactctgttaagaagagctgagggaatgattctcgttttagaattcg 2433
Db 2532 tactgcgatacctcgtgaggtgaagagttccttggagggaataatgctttaacatgatgtgg 2591
Oy 2434 tggagagagctcgcattgttagatgaagaagtgtctcattttgagcagtaatgccttct 2493
Db 2592 agctctctctcattcttaccctgaatacctgcattgttttgaaccatgctccatacat 2651
Oy 2494 gaatttgcagttgtctatgacacatcaagaagtttaagaacaagagacagaagctcg 2553
Db 2652 caactgcagatcgcagctataatagctgacagcctctcggaggaagagacagaaggaag 2711
Oy 2554 tgaatttgaagaatagccgtctgtgaatcttgccttaccatccaggaatccgatttgataa 2613
Db 2712 atccttcttgtagcaagaacctctcaatttacttcttgccttaagggttgaattggaagaa 2771
Oy 2614 ggaatcagagctcgaagatgacagatgacacatcaactctgtgttaacagtgatcttct 2673
Db 2772 gtctcctggttgtaagtactttcttctatgactgcacttaacctatgtccgcactcat 2831
Oy 2674 tctgtgtaaccccgactgtgacacacacactgcgaattgagctgttcttggaataacct 2733
Db 2832 cgcgaatgatacccaatgacactacagcactgttaacagcggacgtcttgggaacctta 2891
Oy 2734 cgttcgaatttggcaagaagcatttagctccttgcgtgaggaagacatatttgcctta 2793
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Oy 2794 ctcaaatcttgaagccttagcgaatttcttcttgaattgagctggtc 2841
Db 2952 tcttatgttgaagtgctgcgcagcttcttcttgaagtctgtgac 2999

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RESULT 10
X06816 standard; DNA: 3200 BP.
X06816;
26-APR-1999 (first entry)
Chlamydia pneumoniae surface exposed protein Omp4 DNA.
Omp4: outer membrane protein 4; surface exposed protein; antigen;
infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
Chlamydia pneumoniae.
Key Location/Qualifiers
CDS 205..2991
/*tag= a
W09858953-A2.

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PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHR1/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX WPI: 1999-105610/09.
DR P-PSDB: W88417.
XX
XX
XX Species-specific test for identifying mammals infected with
XX Chlamydia pneumoniae - comprises detecting antibodies specific for
XX outer membrane proteins of C. pneumoniae or nucleic acids encoding
XX these proteins
XX
XX Claim 6; Page 35-40; 115pp: English.
XX
XX This DNA sequence codes for the novel 98.9 kDa surface exposed
XX protein Omp4 (see W88417) of the human respiratory pathogen
XX Chlamydia pneumoniae. By generating antibodies against C.
XX pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
XX was obtained which reacted with outer membrane proteins. The
XX antibody was used to identify the genes (see X06816-27) encoding
XX Omp4-Omp5 proteins (see W88417-28) in an expression library of
XX C. pneumoniae DNA. The genes are situated in 2 gene clusters:
XX Omp2,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
XX the other, and encode polypeptides of about 89.6-100.3 kDa and
XX about 56.1 kDa. The invention provides a new species specific test
XX for identifying mammals (including humans) infected with Chlamydia
XX pneumoniae. The test comprises detecting antibodies specific for
XX Omp4-Omp5 or detecting nucleic acid fragments encoding these outer
XX membrane proteins, especially by PCR. The proteins are also used
XX in the diagnosis of C. pneumoniae infection in mammals. The
XX nucleic acids and proteins can also be used in the immunization of
XX mammals, the nucleic acids being particularly useful as DNA
XX vaccines for effecting in vivo expression of antigens. The
XX vaccines may also prevent atherosclerosis and bronchial asthma,
XX which are possibly associated with C. pneumoniae.
XX
XX Sequence 3200 BP; 946 A; 708 C; 623 G; 923 T; 0 other;
XX
XX Query Match 15.5% Score 465.8; DB 20; Length 3200;
XX Best Local Similarity 52.0% Pred. No. 5.8e-119;
XX Matches 1172; Conservative 0; Mismatches 1177; Indels 90; Gaps 11;
XX
Oy 296 cctggaacagcagacagacatcaaaaagcgttttaacacactaagaagcgatttgaact 355
Db 394 cctggaacagcagacaccccttatctgacagtggtttaaagcaaacacagcaactctacc 453
Oy 356 ttacaggttaacggaagcctctctatgttccaaacggtgagacaggaactgtgacagg 415
Db 454 ttcttggggaacggtcatalagcttaacggttgccttataagatgctgacacatcagagt 513
Oy 416 gctgtgttaacagcagcgtgtgtatagataatcaccacagttatagggtttcttcgta 475
Db 514 gctgtgtcattacaa---cagcaataaagaactcttactctcagggtttcttactag 570
Oy 476 tctttattgctctcctcgtgaagttcgtataactacccgcaagaagccgtttagctcct 535
Db 571 agttttagtctctcctcagcaacaggttactacagtcagggaagcctt---tcacca 627
Oy 556 acgggtactctgagtttgaacaaaatgctagttgctcttcagcaaaacttttcaag 595
Db 628 gcaagagcgttaaatctagaataatctgtaactctgtagttgctggaatttttctact 687
Oy 596 gataatgcggtgtctatccgcgcaaaactcttcaataacagcagacataatgtacgt 655

```

Dh 688 gcaagatggtgagctatcaaaagagcgtcttctctttaactgacattcgtgagatgct 747
QY 656 ctgttttttgaataactctctcaaaagaagcggagccattcagacttccgatgacct 715
Dh 748 ctttttagtaacactctctcaacaaaggagagcaattgctactacagcagcgct 807
QY 716 accattactggaacaaaggaggagctctctttctgcaactactctctcgatctgga 775
Dh 808 cgcataagcaataaacaaggtatgttagatctcctatctcaatagcgtctacgltcaga 867
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QY 1310 gttaatgagctccggagacttctgcactcaatatcaggggaacatcatcttccacaga 1369
Dh 1372 ataaataacggtctctggtgagctctcaatccatatcaagaacgattcttatctgga 1431
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Dh 1432 gaaaccttaacagagatgaactaaagttgcgtgacaatttlaaaatttcaatccaagcag 1491
QY 1430 cctgttaacttctcaagaggtactctatcttlaaaacatgaggtgactctgcagactcag 1489
Dh 1492 ccagttccctatccgaggaagtattgtctacaagaaggagctacatttagagagacg 1551
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Dh 1552 agcttccctcaaaagcggttctctcctcgagatgattccaagacgaatataatataact 1611
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QY 1607 aagaagggcaaaaatagaacaacaaagctagctcaaaaaatctgacttattctggaaccatc 1666
Dh 1672 cagccggtcagccttaacagaagaagtgctccaataaagtgtcgtatctgtggaagcctc 1731
QY 1667 acttattggaaccgagcggtttttagaatacatcagtttaagaatcctcagctc 1726
Dh 1732 aacctgatgatattgaaagggaacattatgaagaatcatatgttcagccatgaccagctc 1791

QY 1727 taacacatcttaagcgtcaaaagctctcgtgaactgttaacaaagccgcag----- 1775
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Dh 1912 gttcaattggaactcggatcacagatlaaanaataaagaagccacggcaacttggacaaa 1971
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Dh 2272 ttatgcgtacaacaacactcagaaactcagctggtgagacttattctcaagcactcat 2331
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Oy	2768	cgtcgaaggaacccctttttgcttaactcaaattttgaagcctttagccaatttcttt	2827
Db	2872	aggggttagcaacaactcgccttaactccaattcgagctcttcggacattagctatg	2931
Oy	2828	gaattgcgttgggtcatctgcgaattacaatgttagcttagagagcaaaataccattcta	2886
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XX	261508	standard; DNA; 3050 BP.	
AC			
XX	261508;		
XX			
D7	19-JUN-2000	(first entry)	
XX			
DE	DNA encoding the CPN100394 polypeptide.		
XX			
KW	CPN100394; Chlamydia infection; immune response; vaccine; ss.		
XX			
OS	Chlamydia pneumoniae.		
XX			
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FT	CDS	101..2938	
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XX			
PN	MO200011183-A2.		
XX			
PD	02-MAR-2000.		
XX			
PE	18-AUG-1999;	99NO-IB01449.	
XX			
PR	20-AUG-1998;	98US-0097187.	
PR	20-AUG-1998;	98US-0097188.	
PR	20-AUG-1998;	98US-0097189.	
PR	20-AUG-1998;	98US-0097190.	
PR	20-AUG-1998;	98US-0097195.	
PR	20-AUG-1998;	98US-0097196.	
PR	20-AUG-1998;	98US-0097197.	
PR	27-AUG-1998;	98US-0097191.	
PR	17-AUG-1999;	99US-0376770.	
XX			
PA	(CONN-) CONNAUGHT LAB LTD.		
PI			
PI	Murdin AD, Oomen RP;		
XX			
DR	WPI: 2000-224703/19.		
DR	P-PSDB; Y69368.		
XX			
PT	Novel antigens and corresponding DNA molecules that can be used to		
PT	prevent, treat and diagnose disease caused by Chlamydia infection in		
XX	mammals, especially humans -		
PS			
PS	Claim 1; Fig 13A-F; 201pp; English.		
XX			
CC	261507-09 encode Chlamydia pneumoniae polypeptides. The polypeptides		
CC	are present in the bacterial membrane structure, in the external		
CC	vicinity of the membrane structure, in the inclusion membrane		
CC	structure, in the external vicinity of the inclusion membrane structur		
CC	and in the cytoplasm of the infected cell. The polypeptides may be		
CC	used to prevent, treat and detect the presence of Chlamydia infection		
CC	and/or the presence of Chlamydia in a sample. The polypeptides may		
CC	also be used to induce an immune response in a mammal. The vaccine		
CC	vector comprising the polynucleotides is used to induce an immune		
CC	response in a mammal. Antibodies directed against the polypeptides		
CC	may also be used therapeutically to treat and/or prevent a Chlamydia		
XX	infection.		
XX			
Sequence	3050 BP; 897 A; 622 C; 695 G; 836 T; 0 other;		

Query Match	13.0%	Score 389	DB 21	Length 3050	
Seq Local Similarity	50.7%	Pred. No. 1.le-97			
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QY	224	tcaattcttgagatgcaggaagatgcttgcgaactcctcctatttaaggaatgcact	283		
DB	230	tctccgaaatctacacaggaatgctgcgaagaactcctcctctccacagggaggt---	286		
QY	284	ctagaanaatattccctcgagacagccagcaatcccaanaagctttttaacaacacag	343		
DB	287	cgtatatacatgcgggaaaggtggttcattacgaagaacttccttgtagaacctgc	346		
QY	344	ggcgattggaacttccacaggttaacgggaactcctctatggtccaaacggtgcaggg	403		
DB	347	ggcgattctacatttttagtgaatgaataccctaaagttccctgcgtgcagtagcaggt	406		
QY	404	actgcagagaggggcgcgcgtttaaaccgacgctgtgtatgaatataccacgttatagg	463		
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QY	584	aactttcaacgagtaatgycggtgcataccgcaaaacacttctcaataacaggaact	643		
DB	578	aatgcctctgcgaagatgctggtgttttaaggaaactcctgcgtatccagggaatc	637		
QY	644	acaaatgcagctcgttttcttgcgaataactcctcccaagaagaacggcggaaccatcag	703		
DB	638	aaaaatagtcgatttttgcacaataatacatcttcgaaanaagggaggtctccacg	697		
QY	704	tccggtcccttaaccattactcgtgaaacccaaggggaagctcttttctgcacaatacttc	763		
DB	698	actcaaggaactcaacatacagaaataacttaaggacgcgaagttccaatgaaacaaga	757		
QY	764	tccgattctgcagctgcacatttttcaagaagcctcgtgtaattttcctaatacgtcaaa	823		
DB	758	gtgacctcaggaagggcctttagattagagccgctctaatcatcctgcgaaccatgag	817		
QY	824	gttcccttattgacaataagttcaagga--gcgaagctcccaacaaacgggggatatg	880		
DB	818	tgcataatttccacaanaataaagaactcttggaatgctgcgaatgycggccataaatgvc	877		
QY	881	tcaaggaagttgcatactggtgttaaaaact-----	910		
DB	878	tcaagggaccttaacttaactgatacaactcctcttgtaacttcaagaanaataagcacatg	937		
QY	911	-----agtaacagatactaaggttcaacctcaacttgcgaatacaatgta	952		
DB	938	caggaatgtgagctcttgtgtagcacaggaaccataagcattaccggtagtgattcatc	997		
QY	953	ccttcacgaacaataactatgcacaacgccgggaagagctatcctatgynaanaagctcgaa	1012		
DB	998	aatgcatacaggaanaatacttcaganaaaaaagagagaggaattctgcagcttccctaag	1057		
QY	1013	ctgcttcgcgagagacttaccctatcagttcagaaatagtgcaatgaggaagccct	1072		
DB	1058	atttggaagggcagggcgctcctcttcttataaacytaagatcatgccaacct	1117		
QY	1073	aaagtgagccatagcatacgaagatagtgvggaatgagttatccgcgcgaatggt	1132		
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 DB 1466 cagctgctactcttagtgatgagggagagcttagtacttaacagggagtgactgataca 1525
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 QY 2786 tgcttaactcaaattttgaaagccttagcgaatttctttagatggcggtgactct 2845
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RESULT 12
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 ID X06827 standard; DNA; 2838 BP.
 XX
 AC X06827;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Chlamydia pneumoniae surface exposed protein Omp15 DNA.
 XX
 KW Omp15; outer membrane protein 15; surface exposed protein; antigen;
 KW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
 OS Chlamydia pneumoniae.
 OS
 PN W09856953-A2.
 PD 30-DEC-1998.
 PD
 PF 19-JUN-1998; 98WO-DK00266.
 PF
 PR 23-JUN-1997; 97DK-0000744.
 PR
 PA (BIRK/) BIRKELUND S.
 PA (CHRI/) CHRISTIANSEN G.

XX Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygnd P;
PI WPI: 1999-105610/09.
DR P-PSDB: W88428.
XX Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PI outer membrane proteins of C. pneumoniae or nucleic acids encoding
PI these proteins
XX
PS Claim 6, page 70-71, 115pp: English.
XX
CC This DNA sequence codes for the novel surface exposed protein Omp15
CC (see W88428) of the human respiratory pathogen Chlamydia pneumoniae.
CC By generating antibodies against C. pneumoniae outer membrane
CC complex, a polyclonal antibody (PAB 150) was obtained which reacted
CC with outer membrane proteins. The antibody was used to identify
CC the genes (see X06816-27) encoding Omp4-Omp15 proteins (see
CC W88417-28) in an expression library of Chlamydia pneumoniae DNA.
CC The genes are situated in 2 gene clusters: Omp12, 11, 10, 5, 4, 1, 3 and
CC 14 in one cluster and Omp6, 7, 8, 9 and 15 in the other, and encode
CC polypeptides of about 89.6-100.3 kDa and about 56.1 kDa. The
CC invention provides a new species specific test for identifying
CC mammals (including humans) infected with Chlamydia pneumoniae. The
CC test comprises detecting antibodies specific for Omp4-Omp15 or
CC detecting nucleic acid fragments encoding these outer membrane
CC proteins, especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids
CC and proteins can also be used in the immunization of mammals, the
CC nucleic acids being particularly useful as DNA vaccines for
CC effecting in vivo expression of antigens. The vaccines may also
CC prevent atherosclerosis and bronchial asthma, which are possibly
CC associated with C. pneumoniae.
CC
XX
Sequence 2838 BP: 837 A: 591 C: 648 G: 762 T: 0 other:
SO

Query Match 12.6%; Score 378.4; DB 20; Length 2838;
Best Local Similarity 50.5%; Pred. No. 8.8e-95;
Matches 1415; Conservative 0; Mismatches 1276; Indels 111; Gaps 16;

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DB 130 tctccgaatactcaacagagatgctgacgaactactctctccacaggaagt---t 186
QY 284 ctgaanaatatctctgacagcagcacaacacacaaaagctgttttaacacactaag 343
DB 187 ctgttatagatgcgggaagagtggttcaattacagaaactgtgtgtaaacctgt 246
QY 344 ggcggtttgacttccacggtaacgggaactctcatgttccaaacggtggagcagg 403
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DB 538 aaaaatagtgatattttggaacaaatatacattcttcgaanaaaggagggcgttccagc 597
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Db 1786 aatgtgcagatccatcccgaggaaactcaacccgacagcaaatattagaatg99gtg 1845
QY 1886 aaactcgtatattcccaatcccgagcgtatcgctctttagtcccttaagcttaag 1945
Db 1846 cggacagatataccttcggaatcccgaaacggcaaggatctttagtcccaatagccttg 1905
QY 1946 aatgattatagatattagctctctccatcattcttatgtgagactgcaacgaa99gtg 2005
Db 1906 ggttcttctgtatcagcagcgtctatccaaagaatcagtaaatagagccaatctta 1965
QY 2006 caggagacgctgtcttgggtgtgtgtgattatcttaactctccatcaagatagaca 2065
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QY 2366 accaagatatacaacatacctactgttaaggaagctggggaatgataattcgcctta 2425
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RESULT 13
X06819
ID X06819 standard; DNA; 2526 BP.
XX
XX X06819;
XX
XX 26-APR-1999 (first entry)
DT
DE Chlamydia pneumoniae surface exposed protein Omp7 DNA.
XX
XX Omp7, outer membrane protein 7; surface exposed protein; antigen;
KM infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
XX Chlamydia pneumoniae.
XX
XX MO9858953-A2.
XX
XX 30-DEC-1998.
PD
XX 19-JUN-1998; 98WO-DK00266.
PE
XX 23-JUN-1997; 97DK-0000744.
PR
XX
PA (BIRK/) BIRKELUND S.
PA (CHR/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygdin P;
PI
XX
XX MPI: 1999-105610/09.
DR P-PSDB; W68420.
XX
XX
XX Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PI outer membrane proteins of C. pneumoniae or nucleic acids encoding
PI these proteins
XX
PS Claim 6: Page 49-50; 115pp; English.
XX
XX This DNA sequence codes for the novel 89.7 kDa surface exposed
CC protein Omp7 (see W68420) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see X06816-27) encoding
CC Omp4-Omp15 proteins (see W88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12, 11, 10, 5, 4, 13 and 14 in one cluster and Omp6, 7, 8, 9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.

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XX Sequence 2526 BP; 696 A; 495 C; 597 G; 738 T; 0 other;

Query Match 11.3%; Score 340.2; DB 20; Length 2526;
Best Local Similarity 51.18; Pred. No. 3.2e-84;
Matches 1015; Conservative 0; Mismatches 913; Indels 57; Gaps 7;

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DB 619 aaaaactcaactatctctggtgaggaacctatttcaagggaatacagcgctaacg 678
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DB 2521 ttta 2525

RESULT 14

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2000, 22:58:13 ; Search time 298.85 Seconds
(without alignments)
1518.234 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000
Sequence: 1 cgccttacctagtagaggt.....tgtttgctaaacatttc 3000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2-6/ptodata/2/1na/5C.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	36.8	1.2	1269	3	US-08-758-621-11
2	35.8	1.2	1951	2	US-08-487-880A-112
3	35.8	1.2	1951	4	US-08-478-435-112
4	35.8	1.2	1951	4	US-08-337-483-112
5	35.8	1.2	1951	4	US-08-478-373-112
6	35.8	1.2	1951	5	US-08-474-671-112
7	35.8	1.2	1951	5	US-08-483-577A-112
8	35.6	1.2	8532	5	US-08-452-655B-1
9	35.6	1.2	8532	5	US-08-450-582-1
10	35.6	1.2	9606	1	US-07-741-940-1
11	35.6	1.2	9606	1	US-08-289-548A-1
12	35.6	1.2	9606	2	US-08-452-654-1
13	35.6	1.2	9606	2	US-08-370-235A-1
14	35.2	1.2	1120	1	US-08-254-493-3
15	35.2	1.2	1120	2	US-08-408-222B-3
16	35.2	1.2	2411	2	US-07-952-755-1
17	35.2	1.2	2411	2	US-08-443-679-1
18	34.2	1.1	8220	3	US-08-568-459A-11
19	34.2	1.1	8220	4	US-08-487-826B-11
20	34.2	1.1	19124	4	US-08-487-826B-13
21	33.4	1.1	2061	5	US-09-224-024-30
22	33.4	1.1	2061	6	PCT-US94-07902-30
23	33.4	1.1	4383	7	5175085-4
24	33.4	1.1	4383	7	5177307-1
25	33.2	1.1	3455	3	US-08-861-464-3
26	33.2	1.1	3455	4	US-08-396-001-3

27	33.2	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
28	32.8	1.1	3330	2	US-08-149-103-1	Sequence 1, Appl1
29	32.8	1.1	3330	2	US-08-451-883-1	Sequence 1, Appl1
30	32.8	1.1	9919	5	US-08-880-179-1	Sequence 1, Appl1
31	32.6	1.1	1604	2	US-08-694-579-1	Sequence 1, Appl1
32	32.6	1.1	1604	3	US-08-948-155-1	Sequence 1, Appl1
33	32.4	1.1	2694	5	US-08-975-703-5	Sequence 5, Appl1
34	32.2	1.1	2882	1	US-08-393-219-2	Sequence 2, Appl1
35	32.2	1.1	246240	3	US-08-724-394A-20	Sequence 20, Appl
36	32.2	1.1	246240	3	US-08-724-394A-21	Sequence 21, Appl
37	32.2	1.1	246240	3	US-08-724-394A-22	Sequence 22, Appl
38	32	1.1	347	1	US-08-149-695-3	Sequence 3, Appl1
39	32	1.1	347	1	US-08-377-228-3	Sequence 3, Appl1
40	32	1.1	377	1	US-08-149-695-4	Sequence 4, Appl1
41	32	1.1	377	1	US-08-377-228-4	Sequence 4, Appl1
42	32	1.1	464	1	US-08-149-695-5	Sequence 5, Appl1
43	32	1.1	464	1	US-08-377-228-5	Sequence 5, Appl1
44	32	1.1	595	1	US-08-149-695-6	Sequence 6, Appl1
45	32	1.1	595	1	US-08-377-228-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-758-621-11
: Sequence 11, Application US/08758621
: Patent No. 5846821
: GENERAL INFORMATION:
: APPLICANT: Guerintot, Mary Lou, and Elide, David J.
: TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/758,621
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/018,578
: FILING DATE: 29-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Silverl, Jean M.
: REGISTRATION NUMBER: 39,030
: REFERENCE/DOCKET NUMBER: DCI-099CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1269 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1267
: US-08-758-621-11
Query Match 1.2%; Score 36.8; DB 3; Length 1269;
Best Local Similarity 49.0%; Pred. No. 0.46;
Matches 98; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

[illegible]

Query Match	1.2%	Score 35.8	DB 2	length 1951
Best Local Similarity	52.3%	Pred. No. 1.1		
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1      RESULT 2
2      US-08-487-890A-112/c
3      ; Sequence 112, Application US/08487890A
4      ; Patent No. 5708149
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Loosmore, Sheena
7      ; APPLICANT: Aakness, Robin
8      ; APPLICANT: Schryvers, Anthony
9      ; APPLICANT: Chong, Pele
10     ; APPLICANT: Gray-Owen, Scott
11     ; APPLICANT: Yang, Yan-ping
12     ; APPLICANT: Mardin, Andrew
13     ; APPLICANT: Klein, Michel
14     ; TITLE OF INVENTION: Transferrin Receptor Genes
15     ; NUMBER OF SEQUENCES: 147
16     ; CORRESPONDENCE ADDRESS:
17     ; ADDRESSEE: Sam & Mcburney
18     ; STREET: 6th Floor, 330 University Avenue
19     ; CITY: Toronto
20     ; STATE: Ontario
21     ; COUNTRY: Canada
22     ; ZIP: M5G 1R7
23     ; COMPUTER READABLE FORM:
24     ; MEDIUM TYPE: Floppy disk
25     ; OPERATING SYSTEM: IBM PC compatible
26     ; SOFTWARE: Patent In Release #1.0, Version #1.25
27     ; CURRENT APPLICATION DATA:
28     ; APPLICATION NUMBER: US/08/487,890A
29     ; FILING DATE: 07-JUN-1993
30     ; CLASSIFICATION: 435
31     ; PRIOR APPLICATION DATA:
32     ; APPLICATION NUMBER: US 08/175,116
33     ; FILING DATE: 29-DEC-1993
34     ; PRIOR APPLICATION DATA:
35     ; APPLICATION NUMBER: US 08/148,968
36     ; FILING DATE: 08-NOV-1993
37     ; ATTORNEY/AGENT INFORMATION:
38     ; NAME: Stewart, Michael I
39     ; REGISTRATION NUMBER: 24,973
40     ; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jfb
41     ; TELECOMMUNICATION INFORMATION:
42     ; TELEPHONE: (416) 595-1155
43     ; TELEFAX: (416) 595-1163
44     ; INFORMATION FOR SEQ ID NO: 112:
45     ; SEQUENCE CHARACTERISTICS:
46     ; LENGTH: 1951 base pairs
47     ; TYPE: nucleic acid
48     ; STRANDEDNESS: single
49     ; TOPOLOGY: linear
50     ; FEATURE:
51     ; NAME/KEY: CDS
52     ; LOCATION: 1..1890
53     ; US-08-487-890A-112

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RESULT 3
US-08-478-435-112/c
: Sequence 112, Application US/08478435
: Patent No. 5822523
: GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-ping
APPLICANT: Murgin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS.vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:

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NAME/KEY: CDS
LOCATION: 1..1890
US-08-478-435-112

Query Match 1.2%; Score 35.8; DB 4; Length 1951;
Best Local Similarity 52.3%; Pred. No. 1.1;

Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

30 ttcttgactgttctccatctgtgtatctcttaaatatcaaatcaaga 89
1099 TTGTTGACTGCTGTTGCATCGGTTTGCATTTGTTTACTAGAGAAAGTGT 1040
90 tataattacaagaagctctctcccaagttgtatcttcaattgtatctcc 149
1039 GCTTCCCATCAATTAAGGTTCTTTGAGTAATTTTGTCTTCTCCGTTCTGCTGT 980
150 ctgtgtatgtatgtctaccgagacagttt 180
979 CTTTGCACTAATATACCCCAAAACTTTT 949

RESULT 4

US-08-337-483-112/c
Sequence 112 Application US/08337483
Patent No. 3922562

GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jdb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 1..1890
US-08-337-483-112

Query Match 1.2%; Score 35.8; DB 4; Length 1951;

Best Local Similarity 52.3%; Pred. No. 1.1;
Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

30 ttcttgactgttctccatctgtgtatctcttaaatatcaaatcaaga 89
1099 TTGTTGACTGCTGTTGCATCGGTTTGCATTTGTTTACTAGAGAAAGTGT 1040
90 tataattacaagaagctctctcccaagttgtatcttcaattgtatctcc 149
1039 GCTTCCCATCAATTAAGGTTCTTTGAGTAATTTTGTCTTCTCCGTTCTGCTGT 980
150 ctgtgtatgtatgtctaccgagacagttt 180
979 CTTTGCACTAATATACCCCAAAACTTTT 949

RESULT 5

US-08-478-373-112/c
Sequence 112 Application US/08478373
Patent No. 5922841

GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 MIS:v9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 1..1890

US-08-478-373-112

Query Match 1.2%; Score 35.8; DB 4; Length 1951;
Best Local Similarity 52.3%; Pred. No. 1.1;
Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 30 ttcttgactgttcttccatctggtatctcttaaaatcaaatcaaga 89
DB 1099 ttgttgactgttcttccatctggtatctcttaaaatcaaga 1040
QY 90 tataattcaaatgaagctcttcccaagttgtatttcaacttgcatttcc 149
DB 1039 gcttgccatcaatttaaggtttcttgagatatttttgcgttcttgcgtt 980
QY 150 cttgtctatgatgtctaccgagacagttt 180
DB 979 ctttgccactaaatfaccaccaaaaactttttt 949

RESULT 6

US-08-474-671-112/c
Sequence 112, Application US/08474671
Patent No. 6008326

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,671
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS.V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1890
US-08-474-671-112

Query Match 1.2%; Score 35.8; DB 5; Length 1951;
Best Local Similarity 52.3%; Pred. No. 1.1;
Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 30 ttcttgactgttcttccatctggtatctcttaaaatcaaatcaaga 89
DB 1099 ttgttgactgttcttccatctggtatctcttaaaatcaaga 1040
QY 90 tataattcaaatgaagctcttcccaagttgtatttcaacttgcatttcc 149
DB 1039 gcttgccatcaatttaaggtttcttgagatatttttgcgttcttgcgtt 980
QY 150 cttgtctatgatgtctaccgagacagttt 180
DB 979 ctttgccactaaatfaccaccaaaaactttttt 949

RESULT 7

US-08-483-577A-112/c
Sequence 112, Application US/08483577A
Patent No. 6015688

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:

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?      LENGTH: 1951 base pairs
?
?      TYPE: nucleic acid
?
?      STRANDEDNESS: single
?
?      TOPOLOGY: linear
?
?      FEATURE:
?
?      NAME/KEY: CDS
?      LOCATION: 1..1890
?
US-08-483-577A-112

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Query Match	1.2%	Score 35.8;	DB 5;	Length 1951;
Best Local Similarity	52.3%	Pred. No. 1.1;		
Matches 79; Conservative	0;	Mismatches 72;	Indels 0;	Gaps 0;

Qy	30	ttttagctgtttccctccattgtgtatctctctaaatatcaattcaaatcaagta	89
Db	1099	ttctgtgacgcgtgttgcatcgcgtgtgttcattggttttttttagagagaaagtagtta	1040
Qy	90	tataattacaatgaagctctctctcccaagttgtatcttcacattgtcatcttc	149
Db	1039	gcttgccattaaatgaagttctttagaataattttttgtttcttccggtttcttcctgtt	980
Qy	150	cttgtctatgattgtaccagacagatttc	180
Db	979	ctttggcactaaataccocccaaaactttttt	949
Qy			

RESULT 8
US-08-452-

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; Sequence 1, Application US/08452655B
; Patent No. 5783666
; GENERAL INFORMATION:

```

APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THILVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:

TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:

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?
? LENGTH: 8532 base pair
?
? TYPE: nucleic acid
?
? STRANDEDNESS: double
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: cDNA
?
? ORIGINAL SOURCE:
?
? ORGANISM: Homo sapiens
?
? IMMEDIATE SOURCE:
?
? CLONE: DP2.5(APC)
?
? US-08-452-655B-1

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Query Match	1.28;	Score	35.6;	DB	2;	Length	8532;
Best Local	Similarity	57.08;	Pred.	No.	3.1;		
Matches	65;	Conservative	0;	Mismatches	49;	Indels	0;
						Gaps	0;

QY 1397 agctatgagatgcatttataagatataagctcttcacattactatgagatcgaac 1998
Db 760 AGCCGGTTTATCTCTTCTTGTGAGAGACCTCTCTACCTCTGTGCTGGAGCTTAA 701
QY 1397 gaagaggttcagagagacgtagctcttcgtggtgcgtatatactactcttc 2050
Db 700 GCTGTGATACAGAAAGTATGCTCTTTTCATTTGCGAATTTGCGATATTC 647

RESULT 9
116-00-450-

US-08-450-582-1/C
; Sequence 1, Application US/08450582
; Patent No. 6114124

GENERAL INFORMATION:
 APPLICANT: ALBERTSEN, HANS
 APPLICANT: ANAND, RAKESH
 APPLICANT: CARLSON, MARY
 APPLICANT: GRODEN, JOANNA
 APPLICANT: HEDGE, PHILIP J.
 APPLICANT: JOSLYN, GEOF.
 APPLICANT: KINZLER, KENNETH
 APPLICANT: MARKHAM, ALEXANDER F.
 APPLICANT: NAKAMURA, YUSUKE
 APPLICANT: THILVERIS, ANDREW
 TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
 TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
 NUMBER OF SPOUNSES: 102

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: DP2.5(APC)
FEATURE:
NAME/KEY: CDS
LOCATION: 34...8562
US-08-289-548A-1

Query Match 1.2%; Score 35.6; DB 1; Length 9606;
Best Local Similarity 57.0%; Pred. No. 3.3;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1937 agctatggaatgacattatagatatagctctccattatctatggagactgcaaac 1996
DB 793 ACCCGGTTTCATGCTTGTCTGAGATGACCTCTGCTTCTGCTTGGGACTGTAATA 734

QY 1997 gaagggttcaggagacacgctcttttgggtgctgattatctactcttc 2050
DB 733 GCTGTCGATACGAGATGATGCTTTCGATTGCTGAATCTGGCTATTCTTC 680

RESULT 12

US-08-452-654-1/c
Sequence 1, Application US/08452654
Patent No. 5681454

GENERAL INFORMATION:

APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODIN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOF.
APPLICANT: KINZLER, KENNETH
APPLICANT: KINZLER, KAREN F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THILVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20001-4598

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9299
TELEFAX: 202-508-9100

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE ID NO: 1

LENGTH: 9606 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: DP2.5(APC)
FEATURE:
NAME/KEY: CDS
LOCATION: 34...8562
US-08-452-654-1

Query Match 1.2%; Score 35.6; DB 2; Length 9606;
Best Local Similarity 57.0%; Pred. No. 3.3;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1937 agctatggaatgacattatagatatagctctccattatctatggagactgcaaac 1996
DB 793 ACCCGGTTTCATGCTTGTCTGAGATGACCTCTGCTTCTGCTTGGGACTGTAATA 734

QY 1997 gaagggttcaggagacacgctcttttgggtgctgattatctactcttc 2050
DB 733 GCTGTCGATACGAGATGATGCTTTCGATTGCTGAATCTGGCTATTCTTC 680

RESULT 13

US-08-370-235A-1/c
Sequence 1, Application US/08370235A
Patent No. 5910418

GENERAL INFORMATION:

APPLICANT: VOGELSTEIN, BERT
APPLICANT: KINZLER, KENNETH W.
APPLICANT: HILL, DAVID E.
APPLICANT: JOHNSON, KAREN A.
TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DETERMINING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: DC

COUNTRY: US
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,235A
FILING DATE: 01-JAN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.46688
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508 9100
TELEFAX: 202 508 9299

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 9606 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 5q21
FEATURE:
NAME/KEY: CDS
LOCATION: 34..8562
US-08-370-235A-1

Query Match 1.2%; Score 35.6; DB 4; Length 9606;
Best Local Similarity 57.0%; Pred. No. 3.3;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1937 agcttaaggaatcattatagatagctctctccattatcttaagagacgcaaac 1996
DB 793 AGCGGTTTCATGCTTGTTCAGAGATGACCTCTGCTTGTGTTGGAGACTGTA 734
QY 1997 gaagggtgcagagagacgcttttggtgtgtctgattatcttaactttc 2050
DB 733 GCTTCTGATACGAGATGATGCTTTCGATTGCTGATTCGCTATTCTTC 680

RESULT 14
US-08-254-493-3
; Sequence 3, Application US/08254493
; Patent No. 5439886
; GENERAL INFORMATION:
; APPLICANT: IKEYAMA, SHUICHI
; APPLICANT: KOYAMA, MASARU
; APPLICANT: MIYAKE, MASAYUKI
; APPLICANT: SENOO, MASAHARU
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,493
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865552
; FILING DATE: 09-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 085396-1991
; FILING DATE: 17-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 022321-1992
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 41777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200281 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
CELL TYPE: BREAST CARCINOMA
CELL LINE: ZR-75-1
FEATURE:
NAME/KEY: CDS
LOCATION: 112..795
FEATURE:
NAME/KEY: mat peptide
LOCATION: 115..795
US-08-254-493-3

Query Match 1.2%; Score 35.2; DB 1; Length 1120;
Best Local Similarity 57.1%; Pred. No. 1.2;
Matches 64; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 50 ttggtgatctcttaaaatcattcaaaatcaagatatatttacaatgaagct 109
DB 951 TTATGTTTGTCTTTAATCTTCATTCATATTCAGATTGAGCGGGGGGTTT 1010
QY 110 tcttcccgaagtttgatttctacattgctatttcctcttgctatga 161
DB 1011 GCTTGTGTTGTTTATATTATTTTCAGTTGTTTCTTGTGTTATATATA 1062

RESULT 15
US-08-408-222B-3
; Sequence 3, Application US/08408222B
; Patent No. 5776727
; GENERAL INFORMATION:
; APPLICANT: Ikeyama, Shuichi
; APPLICANT: Koyama, Masaru
; APPLICANT: Miyake, Masayuki
; APPLICANT: Senoo, Masaharu
; TITLE OF INVENTION: MONOCLONAL ANTIBODY, POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Pasteo Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,222B
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,493
; FILING DATE: 06-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-079996-1991
; FILING DATE: 12-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-085396-1991
; FILING DATE: 14-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-022321-1992
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.

REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41777-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
CELL TYPE: breast carcinoma
CELL LINE: ZR-75-1
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 112...795
OTHER INFORMATION: E Mat peptide
US-08-408-222B-3

Query Match 1.2%; Score 35.2; DB 2; Length 1120;
Best Local Similarity 57.1%; Pred. No. 1.2;
Matches 64; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 50 ttgggtatctcttaaatataatcaaatcaaatcaaatatattttacaatgaagtcct 109
DB 951 tttaattgtttgttttaattgcttcaatcaatattgacattgtgagcgcgcggttt 1010
QY 110 tcttcccccaattgatttctacattgctatttcccttgctatga 161
DB 1011 ggttgctttggttatattttttcagttgcttttgcctgttatata 1062

Search completed: November 20, 2000, 09:20:50
Job time: 37357 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2000, 20:42:58 ; Search time 1452.46 Seconds
(without alignments)
12772.107 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 3000
Sequence: 1 cgcctaccctagtagaggt.....tgcttgctaaacacttic j000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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6: gb_est6:*
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117:  qb_gss18:*
118:  qb_gss19:*
119:  em_gss13:*
120:  qb_gss20:*
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122:  qb_gss22:*
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124:  qb_gss24:*
125:  em_gss14:*
126:  em_gss15:*
127:  em_gss16:*

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Description:

No.	Score	Query	Length	DB	ID	Description
C 1	50.6	1.7	923	121	CNS01509	AL105699 Drosophila
C 2	49.4	1.6	334	15	A0076383	A0076383 Drosophila
C 3	44.4	1.5	1025	121	CNS01492	AL104216 Drosophila
C 4	43.8	1.5	596	124	FR0019514	AL101240 F. rubripes
C 5	43.2	1.4	1101	121	CNS00887	AL052689 Drosophila
C 6	42.8	1.4	783	121	CNS000A17	AL055833 Drosophila
C 7	42.8	1.4	1201	121	CNS0167M	AL105396 Drosophila
C 8	42.4	1.4	240	15	A0072820	A0072820 Drosophila
C 9	42.4	1.4	1101	121	CNS0039G	AL065921 Drosophila
C 10	42	1.4	900	108	A0744776	A0744776 HS_5506_2
C 11	41.6	1.4	553	19	AW019090	AW019990 f3d5904.x
C 12	41.6	1.4	1101	121	CNS00KRB	AL077903 Drosophila
C 13	41.4	1.4	1101	121	CNS017NE	AL108260 Drosophila
C 14	41.2	1.4	315	27	B126193	B126193 B126193
C 15	41	1.4	529	34	BE225902	BE225902 fa21c12.x
C 16	41	1.4	735	133	CNS04NSM	AL299119 Tetraodon
C 17	41	1.4	1309	35	BE420736	BE420736 HMM002.A0
C 18	40.8	1.4	494	89	A0124208	A0124208 HS_3122_B
C 19	40.8	1.4	564	23	AW643885	AW643885 GM35a01.w
C 20	40.8	1.4	566	111	AQ829160	AQ829160 HS_3112_E
C 21	40.8	1.4	639	121	CNS0170D	AL108367 Drosophila
C 22	40.8	1.4	949	121	CNS000CJN	AL059162 Drosophila
C 23	40.8	1.4	949	121	CNS000JUN	AL076146 Drosophila
C 24	40.8	1.4	1101	121	CNS00E16	AL067654 Drosophila
C 25	40.6	1.4	242	15	A0037868	A0037868 A0037868
C 26	40.6	1.4	959	121	CNS00655	AL062806 Drosophila
C 27	40.6	1.4	975	121	CNS010XM	AL009555 Drosophila
C 28	40.6	1.4	1101	121	CNS002PM	AL062437 Drosophila
C 29	40.2	1.3	652	118	B15488	B15488 345E3_TV CI
C 30	40.2	1.3	964	122	CNS002GJO	AL166413 Tetraodon
C 31	40.2	1.3	1201	121	CNS0163T	AL106259 Drosophila
C 32	40	1.3	524	122	CNS010Y90	AL106259 Drosophila
C 33	40	1.3	577	14	A1937567	AL1937567 fc94h04.x
C 34	40	1.3	942	121	CNS0186S	AL106389 Drosophila
C 35	40	1.3	1101	121	CNS016L1	AL106389 Drosophila
C 36	39.8	1.3	905	121	CNS00KRX	AL107798 Drosophila
C 37	39.8	1.3	940	122	CNS00GSH	AL106770 Tetraodon
C 38	39.8	1.3	988	121	CNS00072R	AL066743 Drosophila
C 39	39.8	1.3	1101	121	CNS000D7	AL075293 Drosophila
C 40	39.8	1.3	1101	121	CNS002ZH	AL097139 Drosophila
C 41	39.8	1.3	1101	121	CNS010OP	AL098371 Drosophila
C 42	39.8	1.3	1176	123	CNS03R83	AL265908 Tetraodon
C 43	39.6	1.3	1028	123	CNS04RDP	AL304186 Tetraodon
C 44	39.6	1.3	1034	121	CNS01541	AL104988 Drosophila
C 45	39.6	1.3	1101	121	CNS001GJ	AL060877 Drosophila

ALIGNMENTS

LOCUS	CNS01509	923 bp	DNA	SSS	26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC				
ACCESSION	AL105689.1 GI:5617836				
VERSION	SSS.				
KEYWORDS	fruit fly.				
SOURCE	Drosophila melanogaster				
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.				
REFERENCE	1 (bases 1 to 923)				
AUTHORS	Genoscope.				
TITLE	Direct Submision				
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)				
COMMENT	- Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CPBH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.				
FEATURES	Location/Qualifiers				
Source	1..923				
	/organism="Drosophila melanogaster"				
	/plasmid="pBeloBAC11"				
	/db_xref="taxon:7227"				
	/clone_11b="DrosBAC"				
	/clone="BAC14B20"				
	/note="end : SP6"				
BASE COUNT	245 a 142 c 100 g 315 t 121 others				
ORIGIN					
Query Match	1.7%; Score 50.6; DB 121; Length 923;				
Best Local Similarity	34.5%; Pred. No. 0.0081;				
Matches 129; Conservative 66; Mismatches 178; Indels 1; Gaps 1;					
QY	29	tttctgctgcttctcctcattggtcgtcattcctccttaaatatcaaatcaaatcaagt	88		
DB	909	TTTTTTTTTTTAAATWATWATTTTATATTTTAAATATATTAATKAAATTTTTTTT	850		
QY	89	atataattcaaatgaagctctctccccaag-ttgatattcacaattgctattt	147		
DB	849	TTTWTWTWWWAMTAADTTTATTKHVMHATGBRKYTTTTTTTATNGAGGTTT	790		
QY	148	cccttgcctcattgctcaccgagacagtttggatccaagtgcgagttcogatggaa	207		
DB	789	TCMRADSNNSNNNSMMMMHMMSSSVSCAAAKGAANCNGMKRMRKMMHNVGAA	730		
QY	208	taaaatgtaattttcagttcgtggaagcaggaagatgctggaacttacctatt	267		
DB	729	AAAAAAMAAAVYAANDKNSGSMGGSGBBSRBAALMGCGACAKATTYTTATT	670		
QY	268	taagggaaatgcactcagaaatatctcgtgaacagcagcaatcacaanaagctg	327		
DB	669	MGAMACAAAMMAAAAAAAAAAAAAAGCAACWAKTAAAGTCTWHMAAATCAAAAAGGA	610		
QY	328	tttaacaacactaaggcgattgacctcagcaggtgaaggaactctcatgttcca	387		
DB	609	ATMMAABNBKBTBKBAATATTGTCTATTGAATCCATWTTTGAAAGAGAGGGGTCTA	550		
QY	388	aaggttgatgcag	401		
DB	549	AGAGTGGGGGAAG	536		

LOCUS	AU076383	334 bp	mRNA	EST	27-JUL-1999
DEFINITION	AU076383 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSA686, mRNA sequence.				
ACCESSION	AU076383				
VERSION	AU076383.1	GI:5607281			
KEYWORDS	EST.				
SOURCE ORGANISM	Dictyostelium discoideum. Dictyostelium discoideum Eukaryota; Dictyostellida; Dictyostelium.				
REFERENCE	1 (bases 1 to 334) Urushihara,H. Developmental cDNA in Dictyostelium discoideum (1999)				
TITLE	Unpublished (1999)				
JOURNAL COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan Email: dd02nuesakura.cc.tsukuba.ac.jp PROJECT = Dictyostelium discoideum cDNA project in Japan. Location/Organiflers				
FEATURES	source	1..334			
	/organism="Dictyostelium discoideum"				
	/strain="AX4"				
	/db_xref="taxon:44689"				
	/clone="SSA686"				
	/clone_id="Dictyostelium discoideum SS (H.Urushihara)"				
	/dev_stage="slug"				
BASE COUNT	173 a	30 c	38 g	93 t	
ORIGIN					
Query Match	1.6%; Score 49.4; DB 15; Length 334;				
Best Local Similarity	48.1%; Pred. No. 0.012;				
Matches 140; Conservative	0; Mismatches 151; Indels 0; Gaps				
OY	29 ttcttgcactggttcctccatctggtgatcctctaataatcaattcaaatcaagt 88				
Db	325 TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTAATTTAAATTATAATTTATT 266				
OY	89 atatatctacaagaagctctctcccgaagtttgattctacattcgcatcttc 148				
Db	265 TTTTATTTT TTTTATTTT TTTTATTTT TTTTCTTAATTTTTCCTTGAGNATTGG 206				
OY	149 ccttgtctatgatgtctaccgacacagtlttggattcaagtcgaahttcgatlgsaat 208				
Db	205 CTATTTTGAAGATTTTCGTACACCCTTATTAGATTGCAAGTTGTTCCAAGAATCG 146				
OY	209 aaaatggttaattcttcagtcgtgagagtcacgaagaatgctgaaattactacctatt 268				
Db	145 AAATGTGGAACTTACCATTTGTATAAGAGATCAGCACAAATGTTAATAACATTAACCAATg 86				
OY	269 aaaggaaatgtcactctagaanaatatctctcgtgaacagcgacacagaalcaca 319				
Db	85 TATTCATTAACGACATTAACAATTAATCAAGCCAAAGTGTAAAGATTACCA 35				
RESULT	3				
LOCUS	CNS014J72				
LOCUS	CNS014J72	1025 bp	DNA	GSS	26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN011 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL104216				
VERSION	AL104216.1	GI:5615827			
KEYWORDS	GSS.				
SOURCE ORGANISM	fruit fly. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Genosope. Direct Submission				

JOURNAL	Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - FRANCE (E-mail : secrefgenoscope.cns.fr)						
COMMENT	- Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CGP (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.						
FEATURES	Location/Qualifiers						
source	1..1025 /organism="Drosophila melanogaster" /plasmid="pBelobAC11" /db_xref="taxon:7227" /clone_1lb="DrosBAC" /clone="BACN11L11" /note="end : 17"						
BASE COUNT	148 a 88 c 6 g 522 t 261 others						
ORIGIN							
Query Match	1.5%; Score 44.4; DB 121; Length 1025;						
Best Local Similarity	42.6%; Pred. NO.0.41;						
Matches	52; Conservative 29; Mismatches 41; Indels 0; Gaps 0;						
OY	27 aattcttgactgttcttcctcattggtgatctcttaaatataatcaaacaaa 86						
Db	MACHMTTATAMMTATWMTWTMTTTTMTTWMTMWMAACAACMWATTCAACATMMAA 659						
OY	87 gtatatattcaacagtagctcttcctccccaagtgttatcttcattgcattt 146						
Db	ATWTAATWTTATACATTTTTTTTTTTTTTCAMTCCRTATATTAATTTWTTTATA 719						
OY	147 tc 148						
Db	720 yc 721						
RESULT 4							
LOCUS	FR0019514 596 bp DNA GSS 10-DEC-1997						
DEFINITION	F.rubripes GSS sequence, clone 031C10Ac3, genomic survey sequence.						
ACCESSION	AL012404						
VERSION	AL012404.1 GI:2678772						
KEYWORDS	GSS; genome survey sequence.						
SOURCE	Fugu rubripes.						
ORGANISM	Fugu rubripes. Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu. 1 (bases 1 to 596) Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranda,Y., Williams,G. and Brenner,S. Direct Submission Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: bhone@phgmp.mrc.ac.uk V_type: phagescript II KS PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.						
TITLE	Location/Qualifiers						
JOURNAL	1..596 /organism="Fugu rubripes" /db_xref="taxon:31033" /clone_1lb="cosmid 031C10" /clone="031C10Ac3"						
COMMENT	113 a 165 c 126 g 161 t 31 others						
BASE COUNT							
ORIGIN							

Query Match	Similarity	1.5%	Score	43.8	DB	124	Length	596
Best Local	Similarity	45.5%	Pred.	No.	0.51			
Matches	135	Conservative	0	MissMatches	162	Indels	0	Gaps
QY	540	gtagcttgagttgcacaaaaaatgctcagttgctcttcacgacaaacctttcaagagata	599					
Db	244	GTAGCTCCAAACCAACACACACACAGGAANAGCANTTGGTCTAATGACTATCTCCGATC	303					
QY	600	atggcgcgtgctatccacgcgacaaactctttcaatacagagacacaaatgctcgtg	659					
Db	304	CTGTAGCTGCTACTGCTGCTACTACTAGCTACTGCTACTGCTACTGCTACTGCTACTG	363					
QY	660	tttcggaataatcctctccaaagaagcgagacattcaagacttcgaatccgaatgcctta	719					
Db	364	CTGTACTGCTGCTGCTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTAC	423					
QY	720	ttacatggaacccaaggagagctctttttctgcacaatactctccgaattctgagctg	779					
Db	424	CTGCTGCTACTACACACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	483					
QY	780	caattttacagaagccctcgcgactatcttcaataatgacaaagtttccattatg	836					
Db	484	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540					

RESULT	5
CNS008VI	
LOCUS	
DEFINITION	1101 bp DNA GSS 03-JUN-1999
ACCESSION	CNS008VI
VERSION	1
	Drosophila melanogaster genome survey sequence TR33 end of BAC #
	BA018114 of Rpci-98 library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
	AL052689
	AL052689.1 GI:4934738

ORGANISM
Eukaryota; Metazoa; Artinropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
AUTHORS
genoscope.

TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segrete@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this micro-organism was funded by the French Government, the

The BDGP is constructing a physical map of the *Drosophila* Genome Project (BDGP). Collaboration with the Berkeley *Drosophila* community and the BDGP end sequence was carried out as part of a

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster and Tribolium castaneum genome projects.

Metanogaster baculoides was prepared by Kazutoyo Oseogawa and Aaron Mammossier in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn dw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```

FEATURES
source      location/Qualifiers
1. 1101     /organism="Drosophila melanogaster"

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/db_xref="taxon:7227"
/clone_lib="RPCI-98"

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BASE COUNT	289 a	112 c	113 d	316 +	371	others
/clone="BACR18314"						
/note="end : TET3"						

ORIGIN	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

Query Match 1.48; Score 43.2; DB 121; Length 1101;

Best Local Similarity 32.1%; Pred. No. 0.9; Matches 97; Conservative 73; Mismatches 125; Indels 7; Gaps 1;

LOCUS	DEFINITION	763 bp	DNA	GSS	03-JUN-1999
CNS000A1S/C	DROSOPHILA melanogaster genome survey sequence				
CNS000A1S	DROSOPHILA melanogaster genome survey sequence				
	BARC21G10 of Rpo1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				

KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 783)

JOURNAL TITLE Genoscope.
AUTHORS Direct Submission
Submitted 02-TIN-1999) Genoscope - Centre National de Genomique

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila genome.

and BDPG is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDPG *Drosophila*

melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Drexel University School of Medicine.

The library is named RSCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY.

isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual clones is available at <http://www.flybase.org>.

and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	Location/Qualifiers
source	1. .783

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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1fb="Rpci-98"

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/clone="BACR2IG10"
/note="end : TET3"

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BASE COUNT	355 a	95 c	98 g	112 f	123 others
ORIGIN					

[illegible]

Oy	200	gatsggaaataaaaatgcgaattttccagtcgtcgagagtcacgaagaatgcggaactacc	259
Db	915	TTTTATTAATATAAAAAAAWTTTATATTWTTTTTTTTTTTTAAAAAAMWTTMAAAAATTTTT	974
Oy	260	taccatttaaggagaaatgcacctctagaanaatttccctgcaaacgaagcagcatcca	319
Db	975	AAAAATTTTMTATTAATTATTATTATTTTAAAAATTTTTTTTTTTTWTWTATATAAAAAAAA	1034
Oy	320	aaaaatgltttaacaacactaa	342
Db	1035	AAAAAAAAATTTATANMWAAMWA	1057
RESULT	8		
AU072820/c			
LOCUS	AU072820	240 bp	mRNA EST
DEFINITION	AU072820 Dictyostelium discoidium SS (H.Urushihara)		Dictyostelium discoidium CDNA clone SSF174, mRNA sequence.
ACCESSION	AU072820		
VERSION	AU072820.1	GI:5179241	
KEYWORDS	EST.		
SOURCE	Dictyostelium discoidium.		
ORGANISM	Dictyostelium discoidium.		
REFERENCE	Eukaryota: Dictyostellida; Dictyostelium.		
AUTHORS	Urushihara,H.		
TITLE	Developmental cDNA in Dictyostelium discoidium (1999)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan Email: d402n@esakura.cc.tsukuba.ac.jp PROJECT = Dictyostelium discoidium cDNA project in Japan. Location/Qualifiers 1..240 /organism="Dictyostelium discoidium" /strain="AX4" /db_xref="taxon:44689" /clone="SSF174" /clone_1fb="Dictyostelium discoidium SS (H.Urushihara)" /dev_stage="slug"		
BASE COUNT	138 a	23 c	5 g 74 t
ORIGIN			
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Best Local Similarity		51.0%;	Pred. No. 0.91;
Matches 100:	Conservative	0;	Mismatches 96; Indels 0; Gaps 0;
Oy	28	attcttgactgttctctccattcgggtatcctctaataatatnaattcaaatcaaag	87
Db	240	ATAGTGTCATGTTTTTTTATTATTATTATTTTTTTTAAAAAATTTAAAGAGATTTTATT	181
Oy	88	tattattacaaatgaagtcctctctcccagaatttgattctacatttgtctattt	147
Db	180	TATTTATTATTAATAAAATATTTTTATTATTATTATTATTATTATTATTATTATTTTAAAAATTT	121
Oy	148	caccttgctatgatctgacacagacagtttgatccaagtgcgagtttcgatggaa	207
Db	120	TTTTTTTTTTTTTTTTCATGAAGGATATTAAAGTGCTGTGATACCAATTAG	61
Oy	208	taaaaatggtatattt	223
Db	60	TTACAATATGTGTTTT	45
RESULT	9		
CNS00396			
LOCUS	CNS00396	1101 bp	DNA GSS
DEFINITION	Drosophila melanogaster genome survey sequence TERT end of BAC #		BACR08K10 of Rpci-98 library from Drosophila melanogaster (fruit

[illegible]

REFERENCE	Emkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sotungnath; Muridae; Murinae; Mus. 1 (bases 1 to 315)
AUTHORS	Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hata,A., Hayatsu,N., Hirozane,T., Horii,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Itawa,M., Kadoya,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomihaga,N., Toyota,T., Tsunoda,Y., Wataniki,A., Watanabe,S., Yamamura,T., Yamane,K., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	RIKEN Mouse ESTs (Kono,H., et al.)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Yoshihide Hayashizaki Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: +81-298-36-9013 Fax: +81-298-36-9098 Email: genome-res@rtc.riken.go.jp, URL: http://genome.rtc.riken.go.jp/ Carninci,P., Mshiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermosensitization and thermostabilization of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Itawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES	Location/Qualifiers
SOURCE	1. 315 /organism="Mus musculus" /db_xref="taxon:10090" /clone="9630012E11" /clone_id="RIKEN full-length enriched, 16 days neonate cerebellum" /tissue_type="cerebellum" /dev_stage="16 days neonate" /lab_host="DH10B" /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15' GAGGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGGAGAGATTCGAGTAAATTAATTAATCCCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
BASE COUNT	94 a 53 c 33 g 135 t
ORIGIN	FLC 1 "

Query Match	1.4%	Score 41.2	DB 27	Length 315
Best Local Similarity	51.6%	Pred. No. 2.1		
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Db	36	atggtttAACCTTTTTCATCATATATTAATGATCTAATFAGAAAGCATTTTAAAG	95	
OY	88	tatatatttaacaeagaagtcctctctccccaagttgattcttcacttgcatttt	147	
Db	96	TACAAAGAATATATATAAAATTTCATTACTCAAAATTTCTTGACCTTGATTTT	155	
OY	148	cccttggctatgattgctaccgagacagtttggattcaagtgcgagtttcgatcgaa	207	
Db	156	GACCTTCCTCCTTAATTCCTTCATAAAATTTCTTTGTCATGATTTGCATCATATGGAA	215	
OY	208	ta 209		
Db	216	CA 217		

RESULT	15
BE225902	
LOCUS	BE225902
DEFINITION	529 bp mRNA EST 06-JUL-2000
	1a1c12.x1 Mouse E10 5 12 5 Pancreas cDNA Library Mus musculus CDNNR
	3', similar to TR:Q98708 Q98708 CIBP INTERACTING PROTEIN CTIP. [1]
	;', mRNA sequence.

ACCESSION	BE225902	
VERSION	BE225902.1	GI:8931138
REVISION	1	

SOURCE ORGANISM	house mouse. Mus musculus
-----------------	------------------------------

REFERENCE
1 (bases 1 to 529)
Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Page, D.,

TITLE	EST	PROJECT
WashU-Harvard Pancreas		
Unpublished (2000)		
Contact: Douglas Melton		

WashU- Harvard Pancreas EST Project
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 Ma 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmellon@biohp.harvard.edu, meadows@fas.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Adminka Meadows
 (meadows@fas.harvard.edu)
 Trace considered overall poor quality
 Seq primer: -400p from glbco
 High quality sequence stop: 1.

FEATURES
source

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/organism="Mus musculus"
/strain="ICR"
/db_xref="taxon:10090"
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/sex="Both"
/tissue_type="Pancræatic Bud"
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/lab_host="DH10b"
/note="Organ: Pancreas; Vector: pSPORI1; Site_1: Not 1; Site_2: Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.47 kb. Primary library, unamplified. cDNA library Preparation: Goulin Chen."
BASE COUNT      129 a      135 c      130 g      135 t

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ORIGIN

Query Match	1.4k	Score 41	DB 34	Length 529
Best Local Similarity	48.9%	Pred. No. 2.8		
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Db	65	gcTATCCTTTATACCTATTACAGAAACATCATTTTATACGAAAAGGGCTGCTCCNG	124	
OY	532	ctcaacggtagctgagattgcaaaaaaagtcagtttgctctcaagcaaaacttcc	591	
Db	125	GTCTACACTCCACTGGATATGTGTCAAGAGCGTATCTTGCTTGCCAAACCTTTGT	184	
QY	592	aacgataatgcyggtgctaacacccgcgaaaaccttcatctaaggaagactacaatg	651	
Db	185	TTTAAACAACCTACAGGGGGTTTAACTGAAAGCATGTATGCAAGCCCAATCTCATGAC	244	
OY	652	agccctggtttctgaaaaataactcctctaagaagaagcgagccat	696	
Db	245	TGCTCTGCTCTTTACTGTGTGGGGCCCAAGAAAACCAATACCTT	289	

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Tue Nov 21 11:10:32 2000

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